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1: EMBO J 1992 Oct;11(10):3521-31

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A mammalian dual specificity protein kinase, Nek1, is related to the NIMA cell cycle regulator and highly expressed in meiotic germ cells.

Letwin K, Mizzen L, Motro B, Ben-David Y, Bernstein A, Pawson T.

Division of Molecular and Developmental Biology, Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto, Ontario, Canada.

Screening of mouse cDNA expression libraries with antibodies to phosphotyrosine resulted in repeated isolation of cDNAs that encode a novel mammalian protein kinase of 774 amino acids, termed Nek1. Nek1 contains an N-terminal protein kinase domain which is most similar (42% identity) to the catalytic domain of NIMA, a protein kinase which controls initiation of mitosis in *Aspergillus nidulans*. In addition, both Nek1 and NIMA have a long, basic C-terminal extension, and are therefore similar in overall structure. Despite its identification with anti-phosphotyrosine antibodies, Nek1 contains sequence motifs characteristic of protein serine/threonine kinases. The Nek1 kinase domain, when expressed in bacteria, phosphorylated exogenous substrates primarily on serine/threonine, but also on tyrosine, indicating that Nek1 is a dual specificity kinase with the capacity to phosphorylate all three hydroxyamino acids. Like NIMA, Nek1 preferentially phosphorylated beta-casein in vitro. In situ RNA analysis of nek1 expression in mouse gonads revealed a high level of expression in both male and female germ cells, with distribution consistent with a role in meiosis. These results suggest that Nek1 is a mammalian relative of the fungal NIMA cell cycle regulator.

PMID: 1382974 [PubMed - indexed for MEDLINE]

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DTSLGNGQMFGNWTFTGLVFTVMVITVTVKMALETHFWTWINHLVTWGSIIIFYFVFSLF
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Sbjct: 601 QLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVIGRCSPTHTSRWSASDPFYTNDRS 660

Query: 1166 ILTLSTMDSSSTC 1177
ILTLSTMDSSSTC
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>P98197 A11A_MOUSE P98197 POTENTIAL PHOSPHOLIPID-TRANSPORTING ATP
Length = 1187
Score = 1290 bits (3339), Expect = 0.0
Identities = 656/1162 (56%), Positives = 842/1162 (72%), Gaps = 77/1162 (6%)

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D+RTIYV ++ P G Y PQ++ DNRI+SSKYT WNF+PKNLFQFRR+ANFYFLIIF
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Query: 136 RSKNIRVGDIIVRIAKDEIFPADLVLLSSDRLDGSCHVTTASLDGETNLKTHAVPETALL 195
+S+ +RVGDIV + +DE FP DL+ LSS+R DG+CHVTTASLDGE++ KTH AV +T
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Query: 196 QTVANLDTLVAVIECQPEADLYRFMGRMIITQME--IVRPLGPESLLLRGARLKNTKE 254
T A++D+L A IEC+QP+ DLY+F+GR+ + + + +VRPLG E+LLLRGA LKNT++
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Query: 255 IFGVAVYTGMEKTMALNYKSKSQKRSAREKSMNTFLIIYLVILISEAVISTILKYTWQAE 314
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Query: 375 DLDLYHEESDQKAQVNTSDLNEELGQVEYVFTDKTGTLTENEMQFRECSINGMKYQE-- 431
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Query: 432 INGRVPEGPPTPDSSEGNXXXXXXXXXXXXXXXXXXXXXFRTPSPENETELIKEHDLFFKA 491
NG+++P+ -D + + + + +LFF+A
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Query: 492 VSLCHTVQISNVQTDCTGDGPWQSNLAPSQLEYASSPDEKALVEAAARIGIVFIGNSEE 551
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